



1/30

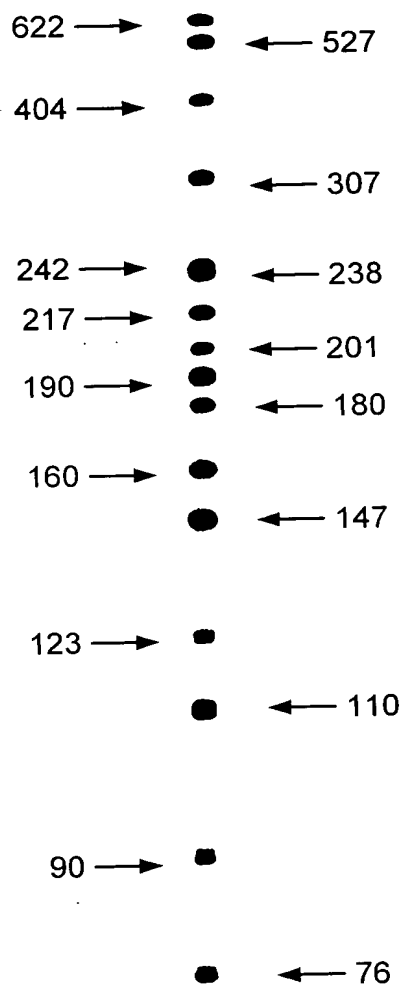


DIAGRAM 1

2/30



FIG. 1A

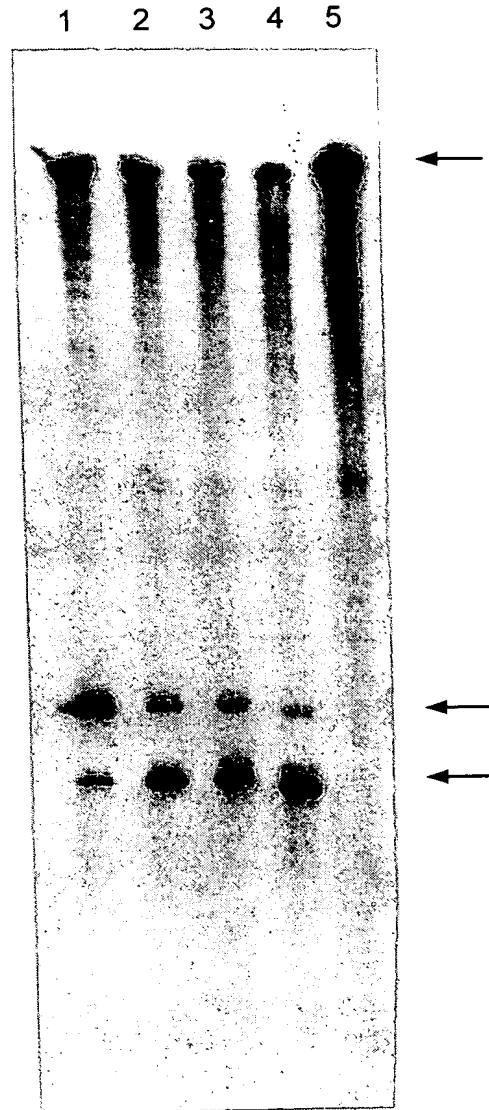


FIG. 1B

3/30

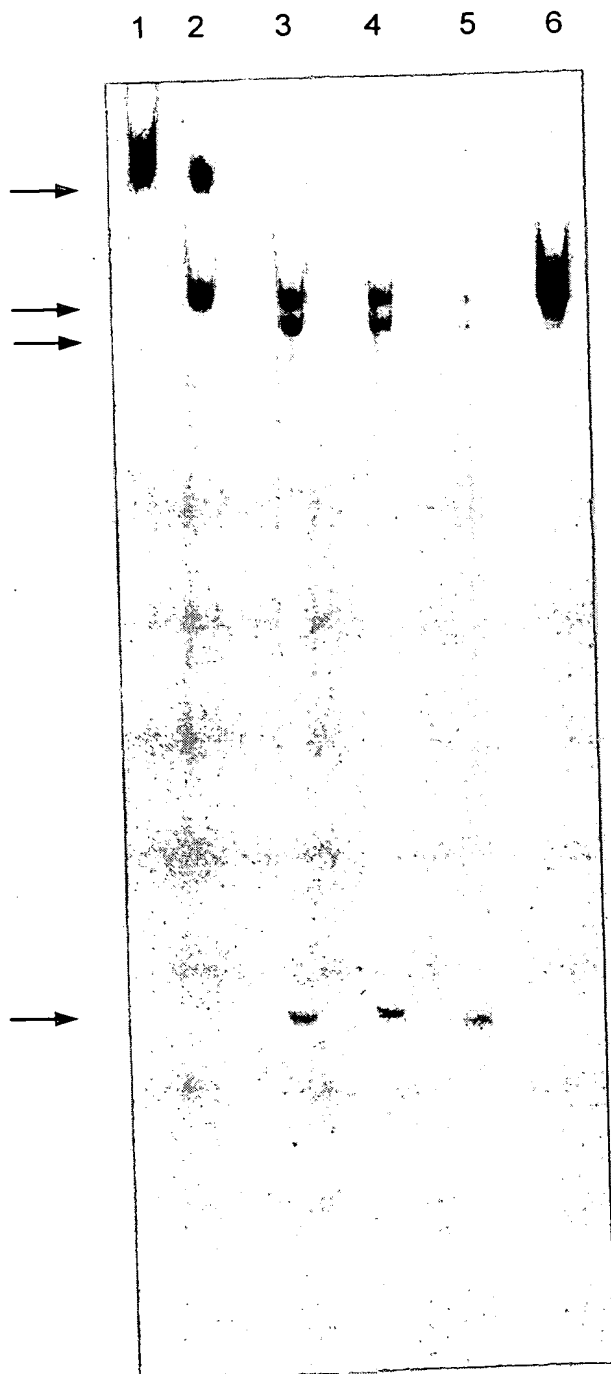


FIG. 2A

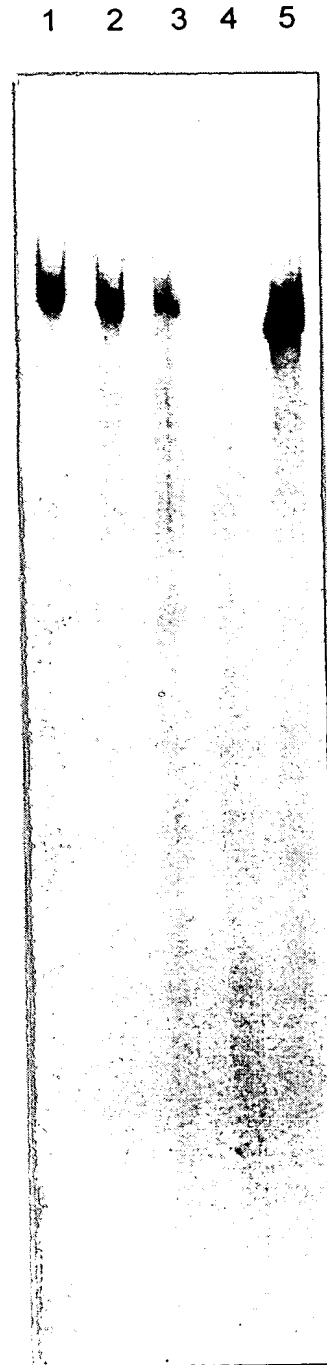


FIG. 2B

4/30

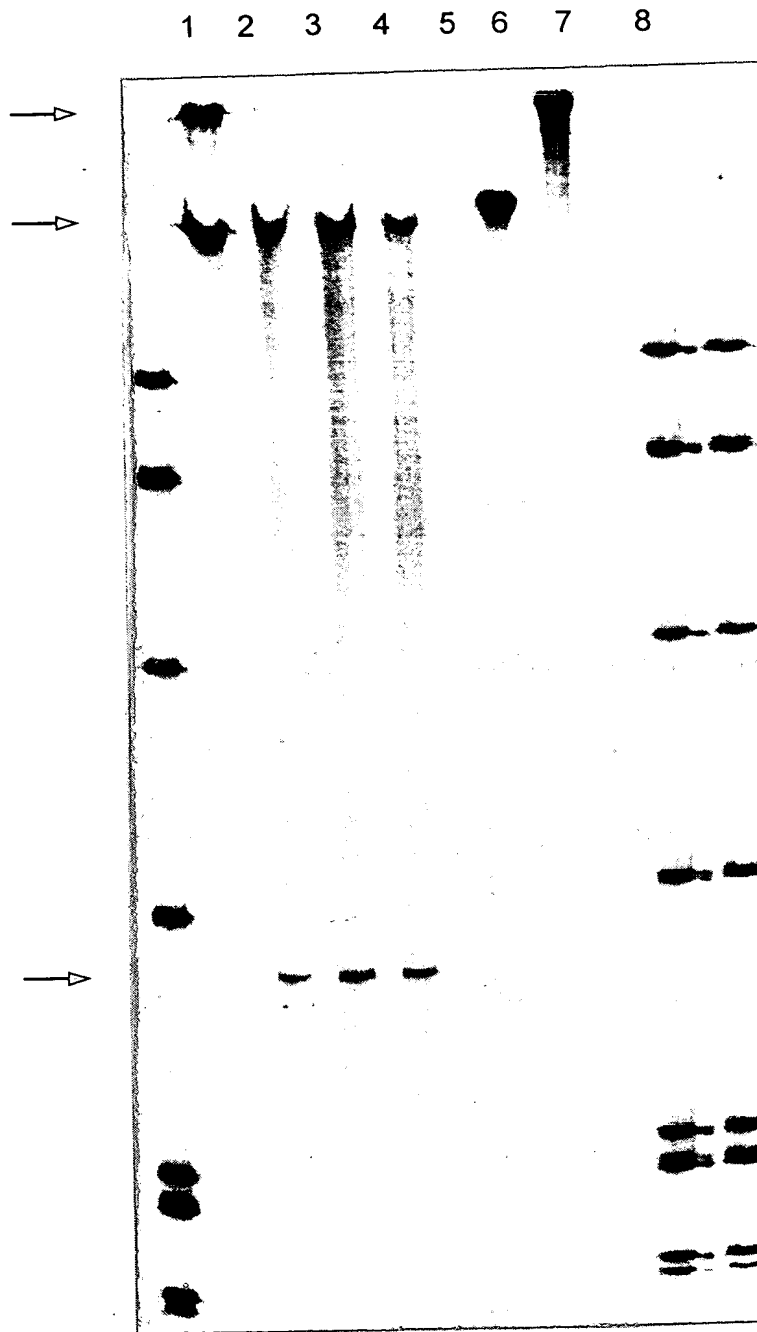


FIG. 2C

5/30

1 2 3 4 5 6 7 8

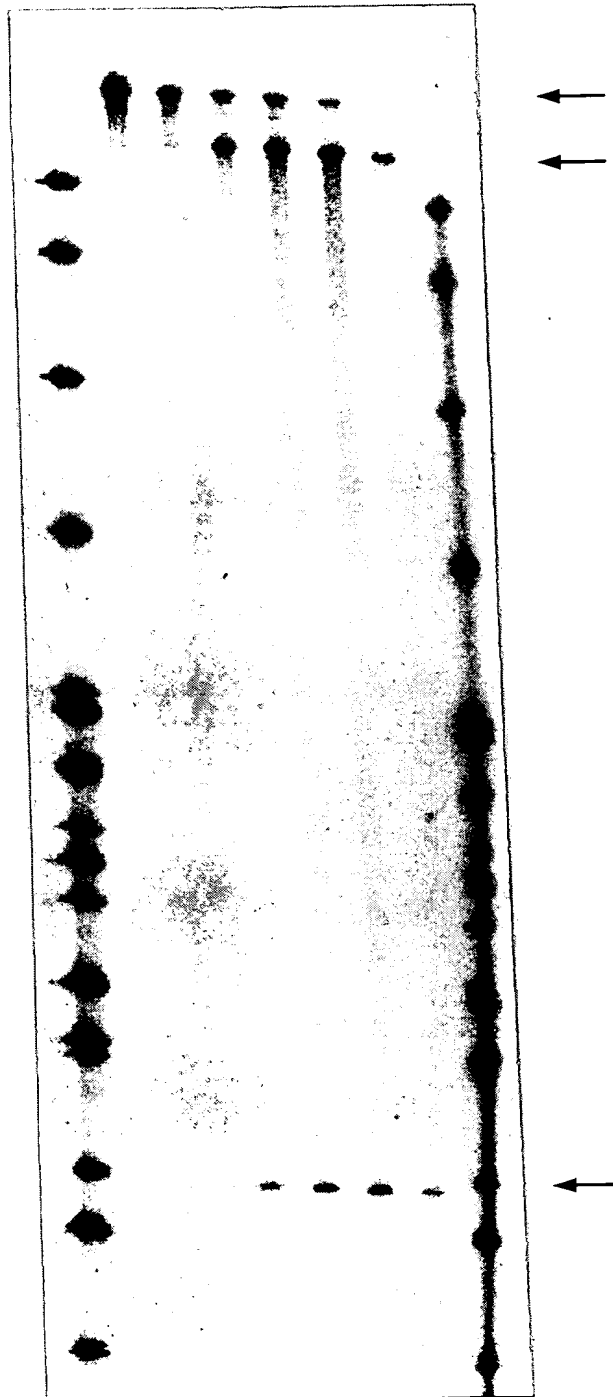


FIG. 3

6/30

1 2 3 4 5 6 7 8

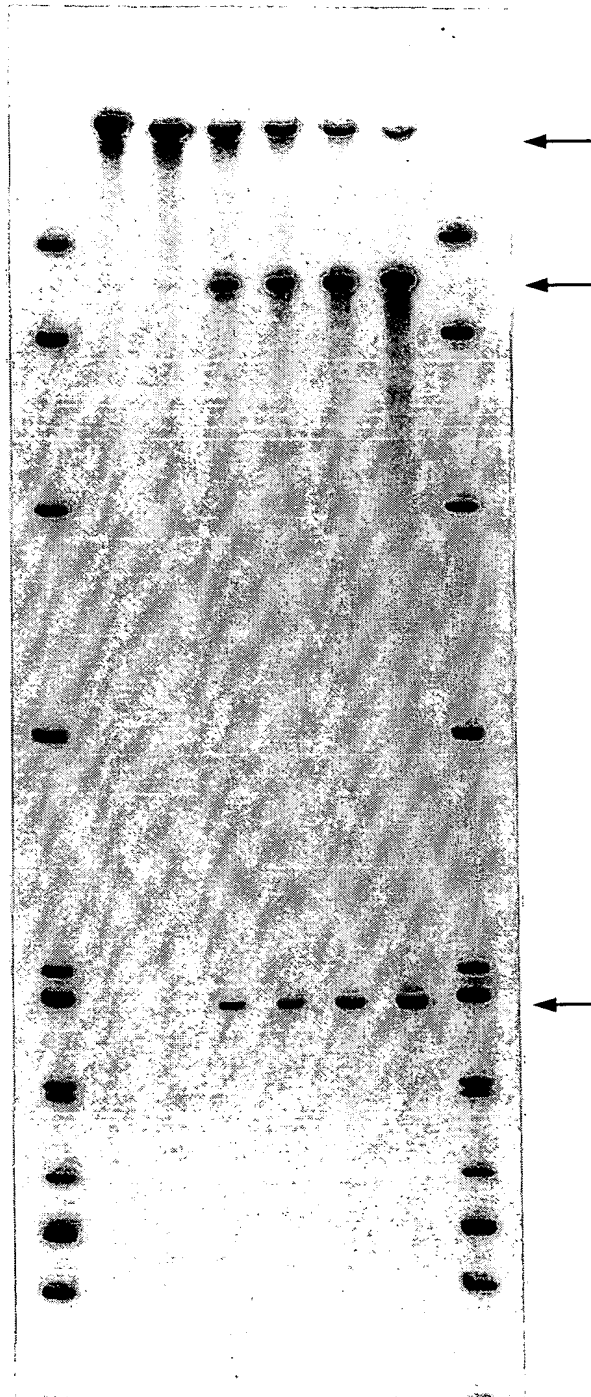


FIG. 4

7/30

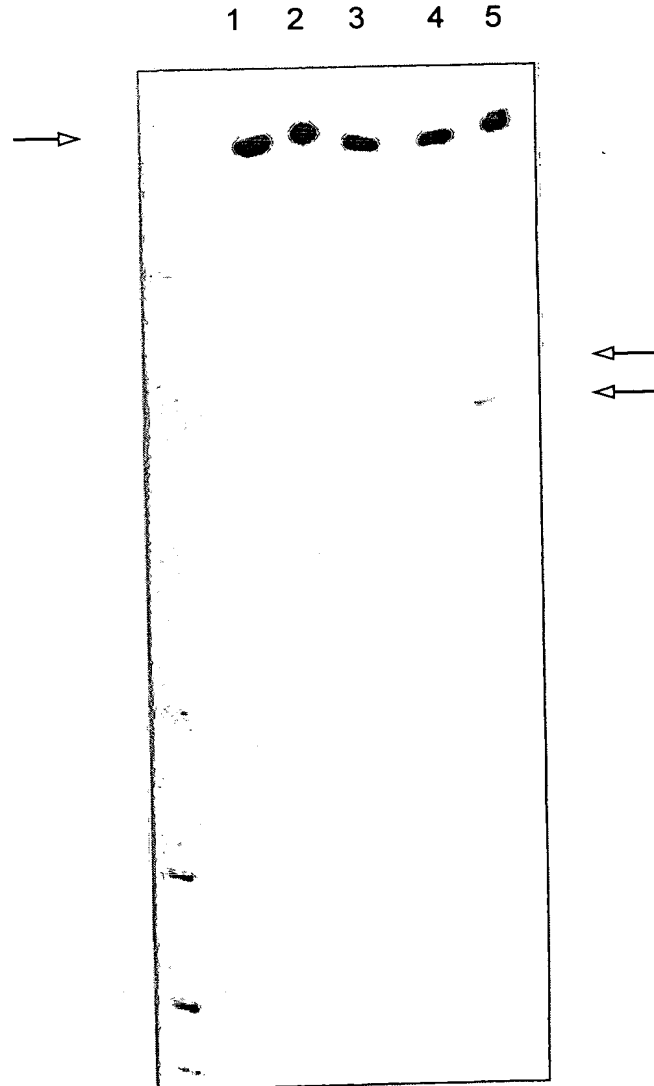


FIG. 5A

8/30

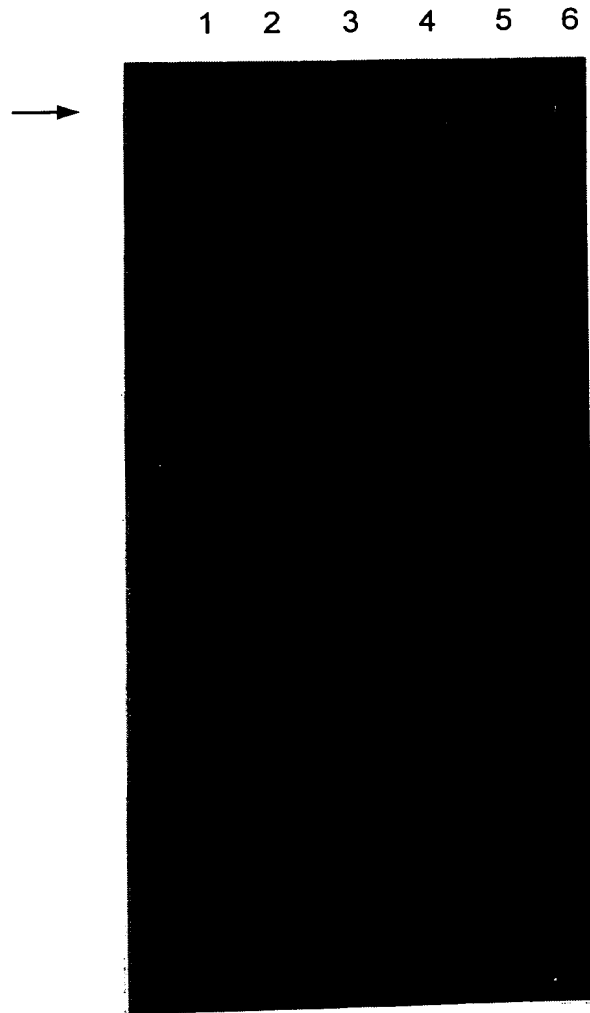


FIG. 5B

9/30

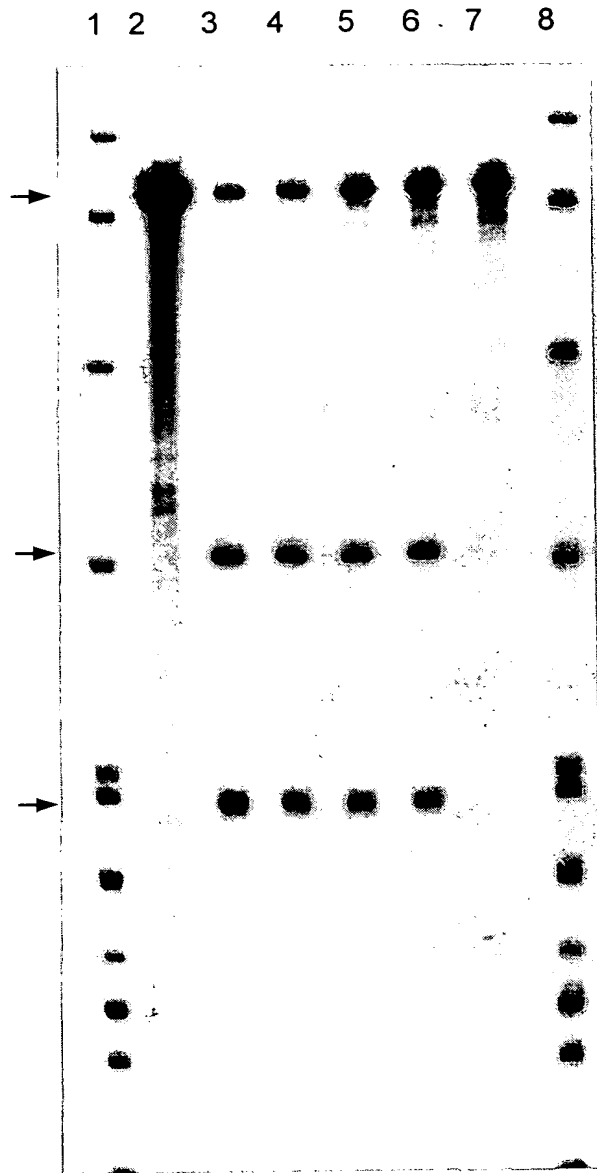


FIG. 6A

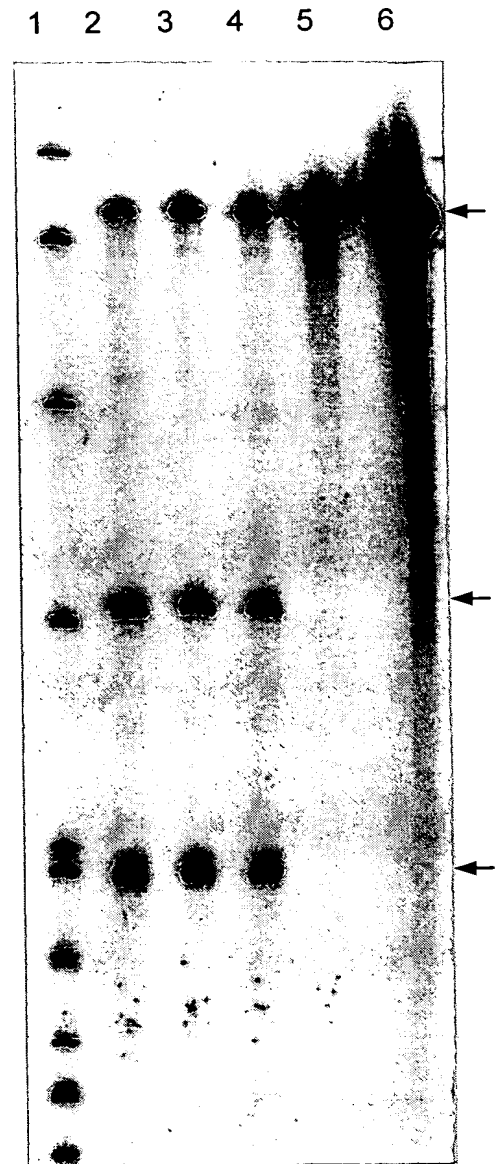


FIG. 6B

10/30

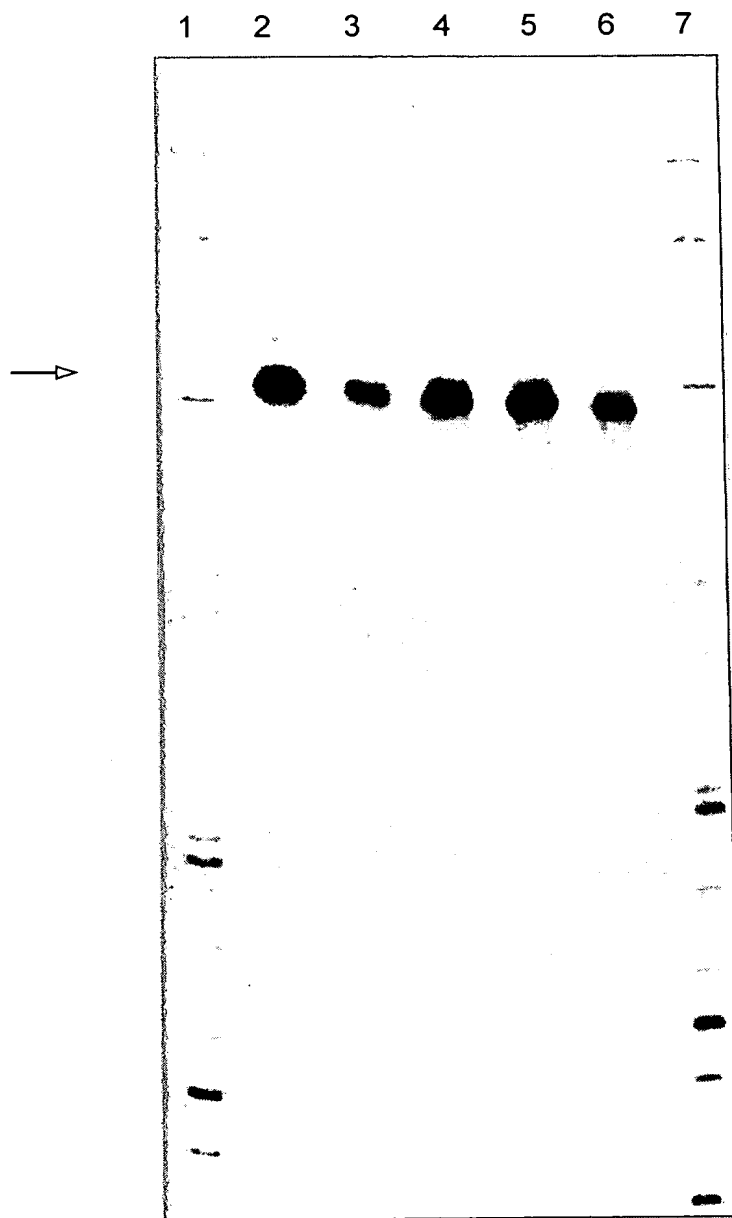


FIG. 6C

11/30

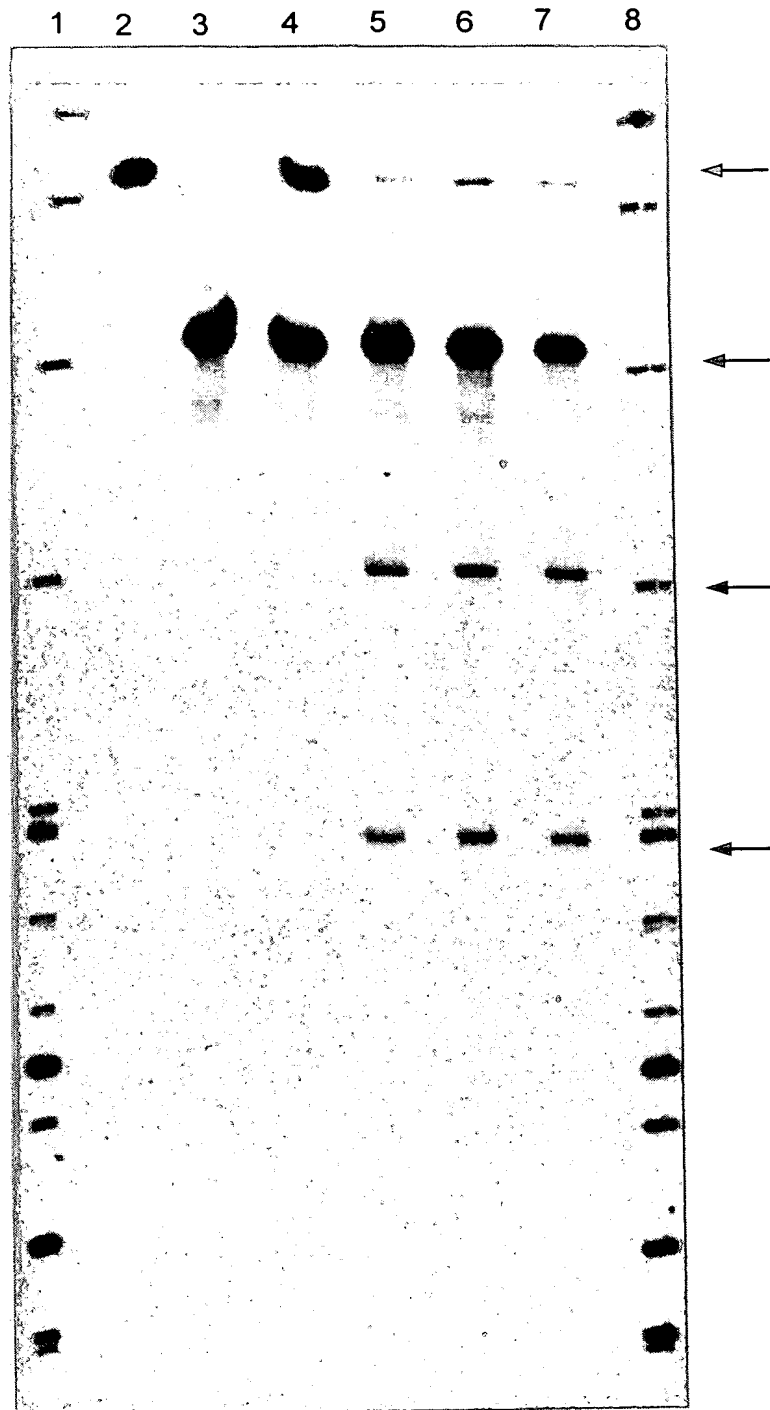


FIG. 6D

12/30

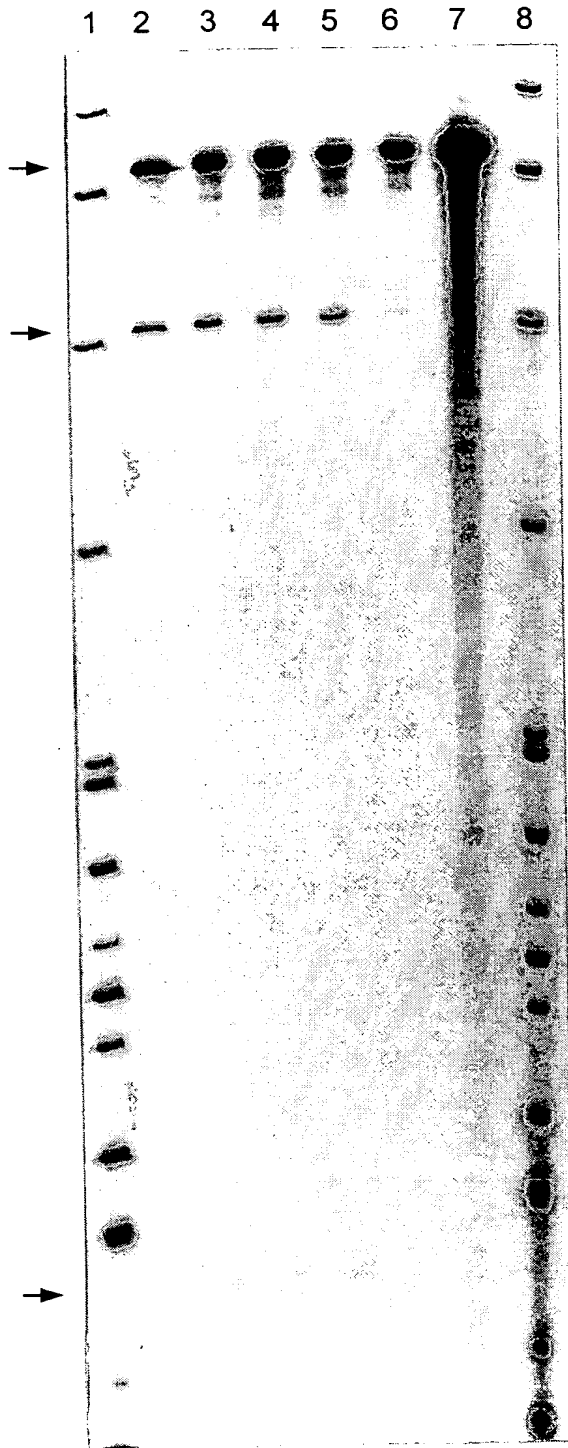


FIG. 7A

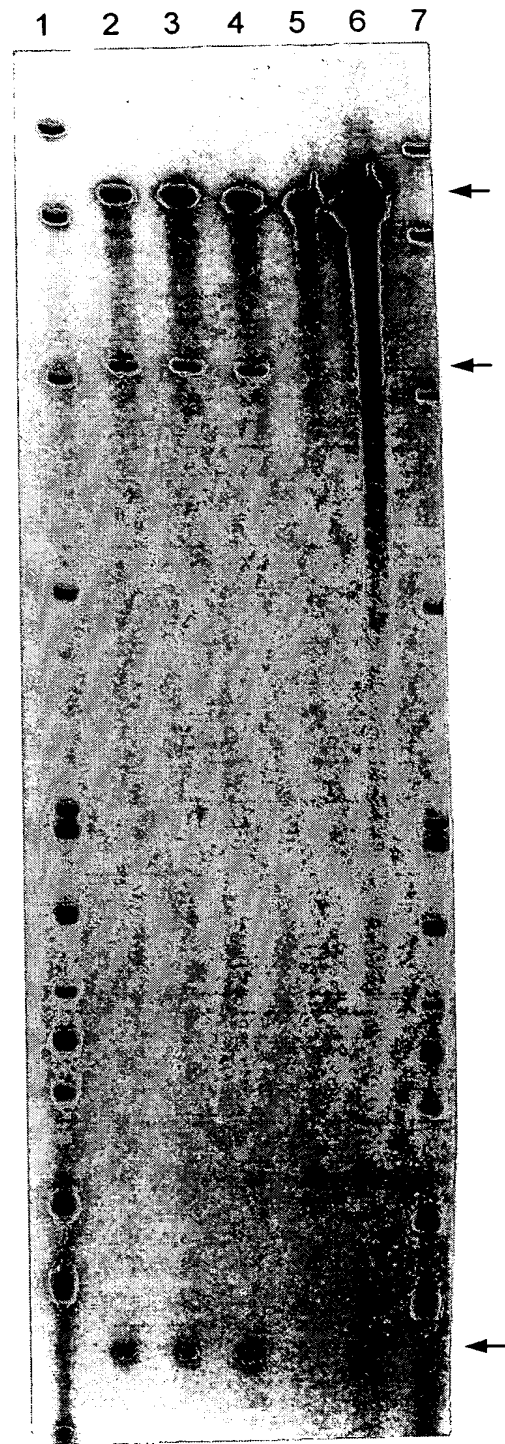


FIG. 7B

13/30

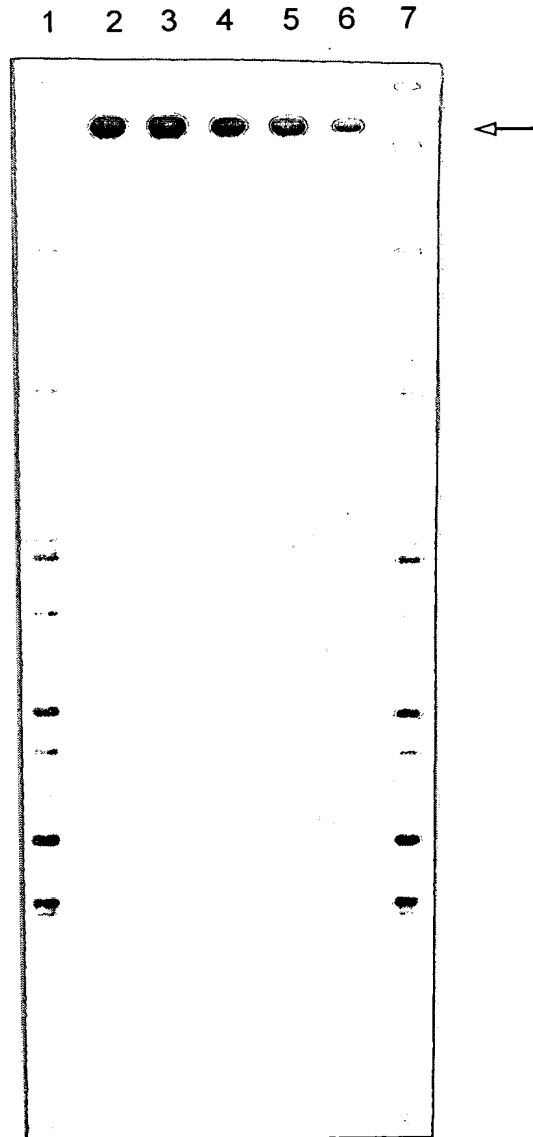


FIG. 7C

14/30

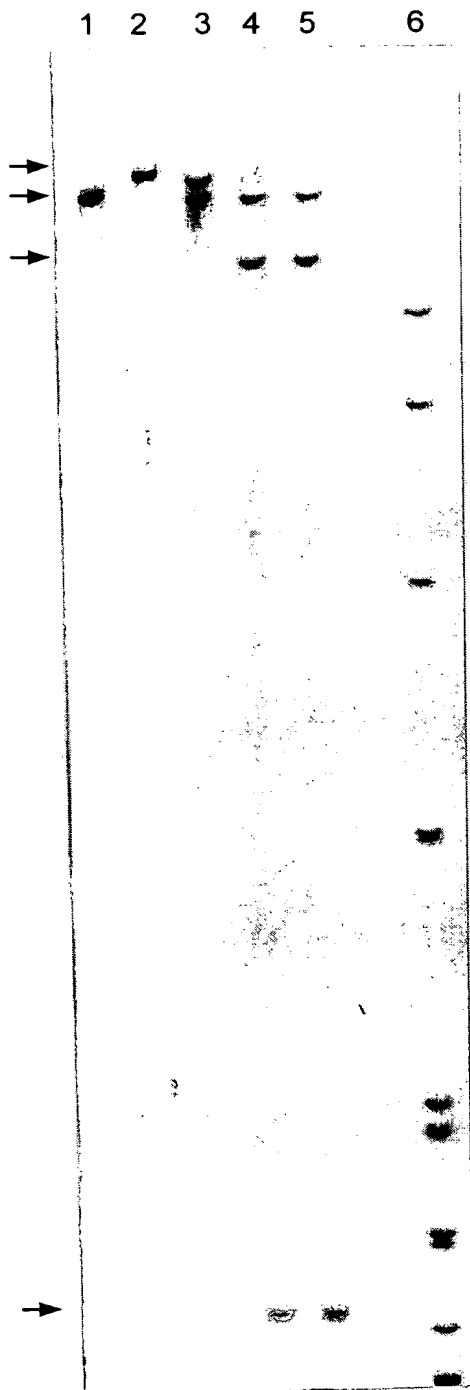


FIG. 8A

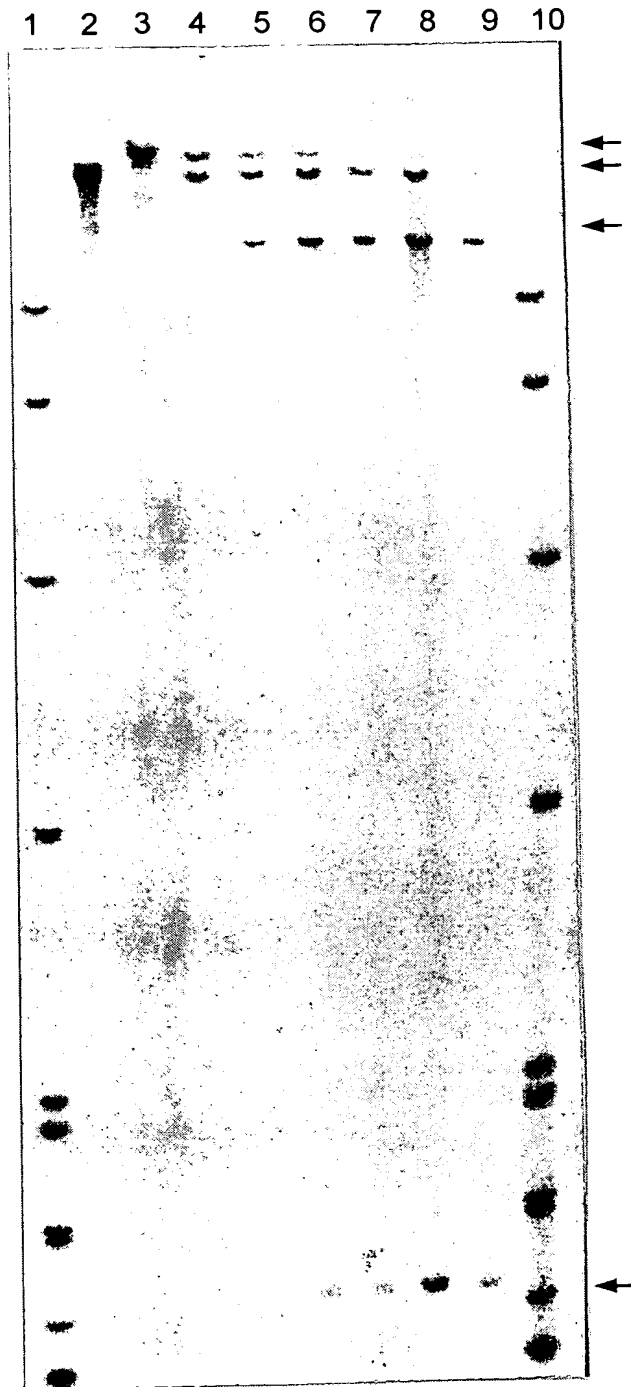


FIG. 8B

15/30

Seq1 Human Rhodopsin

TCCCTTNTGTAGATTGCANNNNCCCAATAAANAAGNCCCGCTTAAAGGCTTATCGAAA
TTAATACGACTCACTATANGGAGACCCAAAGCTTAGAGTCATCCAGCTGGAGCCCTGAGTG
GCTGAGCTCAGGCCTTCGCAGCATTTCTTGGGTGGGAGCAGCCACGGGTCAAGCCACAAGGG
CCACAGCCATGAATGGCACAGAAAGGCCCTAACTTCTACGTGCCCTTCTCCAATGCGACGG
GTGTGGTACGCAGCCCCCTTCGAGTACCCACAGTACTACCTGGCTGAGCCATGGCAGTTCT
CCATGCTGGCCGCTACATGTTTCTGCTGATCGTGTGGGCTTCCCCATCAACTTCCTCA
CGCTCTACGTACCGTCCAGCACAAAGAAGCTGCGCACGCCCTCTCAACTACATCCTGGCTC
AACCTAGCCGTGGCTGAACTCTTCATGGTCCCTANGTGGCTTCACCCAGCACCTCTACANCT
CTCTGCATGGATACTCGTCTTCGGGCCCCACAGGATGCAATTGGANGGCTCTTTGCACCTG
GNGGGAAATTGCCCTGTGGTCCCTNGTGGTCNGGNCACCAACGTAAGTGGTGTNTANCCC
AGAACAACTCCGCTCCC

16/30

seq2 mut447

GGNNNTTGGTCGCGCATTAAGAACTCANGNCCCGCAGCAATCTTGGTGGGAGCAGCTACGGGTGAGCCACAAAGG
CCACAGCCATGAATGGCACAGAAAGCCCTAACTTCTACGTGCCCTTCTCCAATGCCACGGGTGTGGTACGCAGCCCCCTTC
GAGTACCCACAGTACTACCTGGCTGAGCCATGGCAGTTCTCCATGCTGGCCGCTACATGTTTCTGCTGATCGTGTGGG
CTTCCCCATCAACTTCCCTCACGCTCTACGTGACCGTCCAGCACAAAGAGCTGCGCACGCTCTCAACTACATCCTGCTCA
ACCTANCCGTGGNTGAACCTTTCATGGTCCTAGTGGCTTCAACCAACCTCTANACCTCTCTGCATGGANACTTCNTC
TTCCGGCCCCACAGGATGCAATTGGAAGGNTTCCCTTAACACCCGGGGGAAATTCCTGTGGTCCCTGTGGTCCG
GNCANCAACGGTACTTGTGGTNTTAANCCATAAACAAATTCGGCTTCGGGAAAAACATGCCANCNTGGGGTTTCCCTCA
CTNGGTTANGGCGGCTGCCCCACCCCAATCCCNCGGTNGTCAANTAAATCCCAAGGCNNANTGNCNTTTTAAACAAAA
AANNCCCANNTGAGGNGNAAAAATTTTTTTNNCCAANTTTNNNNNNNNNNNTTTTGNNGCTTCCCNCCNANNA
AAATNTTTNNTTTNGNNCCCTCCCCCNCNGAGGCGCCCCNGATTNCCCAAAAGGAAAAAGGCCCGGCCCTNCCN
TTNGGGGGGGCCCNNTNTTTTTTTTCCCNCGGGGTNNCCNTTAAAAANNNTTTTNAAAACCCNTNNCTTTTTTTAA
AAAAACNNANCCCCCCCCNNGGNAAGGC

17/30

seq3 Pro23Leu

NNNTTAGGNCGGATGTCNATATAAGCAGANCTCTCTGGGCTAACTAANAAGAACCCACTGGCTTACTGGCTTATCGAAA
TTAATAAGACTCACTATAGGGAGACCCCAAGCTTCGGAAAGCCCTGAGCTCAGCCACAAGGGCCACAGCCATGAATGGCAC
AGAAAGCCCTAACTTCTACGTGCCCTTCTCCAATGCGACGGGTGTGTACGAGCCTCTTCGAGTACCCACAGTACTACC
TGGCTGAGCCATGGCAGTCTCCATGTGCGCCGCTACATGTTCTGCTGATCGTGTGGCTTCCCCATCAACTTCCTC
ACGCTACGTACCGTCCAGCACAAAGAGCTGCGCACGCCCTCTCAACTACATCCTGCTCAACCTANCCGTGGCTGAACT
CTTCATGGTCCCTANGTGGCTTCACCANACCCCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGGCCACAGGATGCA
ATTTGGAAGGCTTCTTTGCANCTGGGNCGGAAATTGCCCTGTNGTCCCTGGTGGTCCCTGGCCATCAACNGTACTTGTGT
NTNTTACCCATNAACAAATTCGGCTCCGGGAAACATGCACATGGGNTTGCCTCACTNGGTCTGGGCGGCGCCACCC
CACCCCGGTGGTCANTTATCCCANGGCGNAATGCCCTTNANNAAATAACCCACCGAGGTANAAATTTNTTTTATTT
TTGCCCNCCNCCAAANATTTTNTNGGGGGCCCCCNNAANNTTTNNNGNNNNCCNGGGGGCCNCCGNTTC
CCNAAGGAAAGNCCCGNCCCGCCNTCCNTTGNCCNCTGTAAATTNCCNGGGGTGNTTNTNAAANNTTTTANAAAC
CCNCCCTTTTNNNAAAAAANNCNNNCNCCCCCNNAANNGAANNTCTCTTAAAAAANTCGCCAAANANTTTNANTT
NCCCCCCCCCCCCCN

[illegible]

19/30

Seq5

CNCCCCGCCNNTTNAANAANCCNAGCCTCTGGCNAACCTANANAACCACCTGCTTACTGGCTTATCNAAATTAATACGAC
TCACTATAGGGAGACCAAGCTTTACTCGAACTGATGAGTCCGTGAGGACGAAANGCTGCTCTANANGGCCCTATTCTAT
ANTGTACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCCTTCTAATTGCCAGCCATCTGTTGTTGCCCCCTCC
CCCGTGCCCTTCCTTGACCCCTGGAAGGTGCCACTCCCACCTGTCCCTTCTAATAAAATGAAGATNTTNCATCNCATTGTCT
GAGTAAGTGTCAATCTATTCTGGGGGTGGGTGGGCACGACANCAANGGGAAGATTGGGAAAAAATANCAGGCNTGC
TGGGATNCCGTGGGCTCTATNGCTTCTGAAGCGGAAAAACAACCTGGGCTCTANGGGTATCCCCCCCCCTGTAAAC
GNGCATTAAACNCGGGGTGTTGTGGTTACCCCAACTTAACGCTANCTTGCAACGCCCCNAACGCCCCCCTTCCCTTCT
CCCTTCCCTTCNCCCACTTTCGGGTTCCTCCNTCAACCCNAATCGGGGCCCTTAGGTCCAATTATGCTTCGGCCCCNCCCN
AACTAATAGTNGGTTCTTNGCCCCCCNAAAANTTNCCCCNATTGATCCTCCNNAANAACCTTCCCCGAAAAANA
CCCCCCTCANNNCNTCTNCAANNANNNCCCCCNCNTTTTATAAGGATNCAACCCCTTTTAAANANAAAAATACAAAT
CTTNTTTTGTGGTTNCCCCCCCCCAAAATNCCCCCTTCTCCCTTTTCCCCCCCCCAATAACTCTNTTTNCAATNCC
CCCCCCCCCNCNTCNCNNNNNNNTCTTTTNTTNNCCCCCTCCCNATNNTTTTNTTCCCCNCCTCCCCCCCCCCCC

20/30

Seq 6 mouse rhodopsin

TCAGTGCCCTGGAGTTGCGCTGTGGGAGCCGTCAGTGGCTGAGCTCGCCCAAGCAGCCTTGGTCTCTGTCTACGAA

21/30

seq7 m rho mut 1460

NNNTCTTCCNCTTTCGTTTGTGNANANTCANNAAANANAGCGNCCCGGAAGGTGTCAGTGCCCTGGAGTTGCCGCTGTG
GGACCCGTCANTGGCTGAGCTCGCCAAAGCAGCCTTGGTCTCTGTCTACGAAGAGCCCGTGGGCAGCCTCGAGAGCCGCA
GCCATGAACGGCACAGAGGGCCCCAATTTCATGTGCCCCTTCTCCAACGTACAGGCGTGGTGGGAGCCCCCTTCGANCN
TCCGCACTACTACCTGGCGGAACCATGGCAGTTCTCCATGCTGGCAGCGTACATGTTCTCTGCTCATCGTGTGGGCTTCC
CCATCAACTTCCTACGCTCTACGTACCCGTACAGCACAAAGAGTGGGCACACCCCCCTCAACTACATCCTGGCTCAACT
TGGCCCGNTGGGNTTGGAAACCTCCTTCCCATTTGGGTCNTTCCCGGAANGGANTNACCAACCCCTCTAACACATCAA
CTCCCATGGGCTACTTCGTTCTTTTGGGCCCCNAGGCTGTTAATCTCGAAGGCTTCTTTGCCACACCTTGGAAAGTGAA
ATCNCCTGTGGTCCCTGGTGGTCNTGGCCATTAAAGCTACTTGTGGTCCCTGCAACCCCAATAACAATTCCGCTTCCGGG
GAAAANNACCCNCCATGGGTTTGGTCNTCCCNNGANTTAAGGTTNGGNCNTNNNGGCCCCCCCCCCTTGGGNNGTC
CANNTNATTNCCCGANGGNGCCATT

22/30

seq8 RIB33

TCCCCCTNNNTTTTGTAGCNCTGCCAANAAAAAGGCCAGCTCACAGGANAANTANANAACCCACTGCTTACTGGCTTANC
NAAATTAAATACGACTCACTATAGGGAGACCCCAAGCTTGGCACATCTGATGAGTCCGTGAGGACGAAAAAATTGGTCTACA
GGCCCCATTCTATAATGTCACCTAAATGCTANAGCTCGCTGATCATCCTCNACTGTGCCTTCTACTTGCCAGCCNTCTN
TTGTTTGGCCCCCTCCCCCGTGCCCTTCCCTTGACCCCTGGAAGGTGCCACTCCCCACTGTCCTTCCCTAATAAATGAGGAAATT
GCATCGCATTGTCTGAGTAAGTGTCAATCTATTCTGGGGGGTGGGGTGGGCAGGACNNCAAGGGGAAGATTGGGAAAT
ACAATANCCAAGGANCNCTCCCCCNCGGTAATTGCGGATTNGGCTCTNTCGCTTCCTTAAGGCNGAANAACAACACTNGG
GCGCTNCGGGTTTCCCCCNCCNCCCTNTTAGCNCGGCATTANTCGCCGCGGGTGTGTGTACTCCCCACCTNAACG
CTACANTTGCCAGCGCTAACGCCCCCCCCCTTNCNTTCTTCCCTCCTTCTCNCACTTCCCCGGCTTCCCCCNCCANCC
NAAATCNGGGGNCNNAGGTCNCCAATTANTGCTTANGCCCCCCCCCACTTAATTNNGTTNTGTTCCTTTTA

23/30

seq9 HUM RDS

NNTTGGTNCAGTNGGATGTCTATATAAGCAGAGNCTCTGGCTAACTAGNAGAACCCACTGCTTACTGGCTTATCGAA
ATTAATACGACTCACTATAGGGAGACCCAAAGCTTGGTACCGAGCTCNGATCCACTAGTACGGCCGCGCAGTGTGCTGGAA
TTCCTCAGCGCCACGACGAGTGAATACTCCCTGCTCAAGCTGTGATCCGAGACCCCTGCCACTACTGCATTCCACG
GGGATCCCANGTAAATGGGACTCGACATGGGTGCCCCCACGGCANCTCCCTACANCTTGGGCCANCTNCACTTTTCCC
AAAGNCCTAAATCTCCGCTCTCGGCTCCTTAANGTTNGGGTGGGANCCTGTGCTGTGGAAACAACCCAGAANANACT
TGGCAGCATGNGCTACTGAAAGTNCATTTTGAACAGAAATAACGGTCCANTTTGGCCCAAGNNCNGNTCCTAAANT
GGTTCCTCCTNTTTGGTNGNNTCCNCNCTTTCCNCCTNGGAATGTTCTGAAAAATTNAACNCCAAAAAGAACAAATG
AAAAATANTTCTNAAAAACCTTTTGTNCCCCCCCCCNATTTTNAATNAANCCCCNNNNNNNNNNNNNNNNNNCNGGNT
GGGAAATTTTNNNNAANCCCCCCCCCNATTTTNAATNAANCCCCNNNNNNNNNNNNNNNNNNCNGGNT
TTTNTTCCCCCAANNCCCCCTTTTGGCCCTNNGNTTTTNNNGGGCGGGNAAACCGGGGGNAAANGTTTNTNA
NNAACCCCTTTTAAAAAANNANTTNTTTTNTNNNGNNTTTGGAGGTAAAAANNNNCCCCCNNTTNCNAAAA
AAAAAANAANNNGGGGGNGTTCNNNNNNNNNNNNNNNNNNCNCCTTANNNNNNNNNNNNNNNNNNNNNNNTN
NNTTNTNNGTNCNCCCN

[illegible]

25/30

seq11 h per mut (359)

TTTTNTGGNTNTCNAATTAAACGACTCACTATAGGGAGACCCAAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGC
CGCCAGTGTCTGGAATTCTTCANCGCCAGGACCAAGACTATCCCCCTGCTCAAGCTGTGATTCGAGACCCCTGCCACC
ACTACTGCATTACGGGGATCCAGGCTAGTGGACTCGACATGGTAGCCCCAGGGCAGCTCCCTACAGCTTGGGCCA
TCTGCACTTTTCCCAAGGCCCTAAGTCTCCGCCCTCTGGGCTCGTTAAGTTTGGGTGGGAGCTGTGCTGTGGGAAGCAA
CCGGACTACACTTGGCAAGCATGGCGCTACTGAAAGTCAAGTTTGACCAAGAAAANCGGTCAAGTTGGGCCCAAGGGC
TCTGGGCTCNATGNAAACCTNGGTTTCCCCCCCCCTNTTTGGGCTGGGCATCATCTTTAGCCCTGGGANTGTTCCCTG
AANATTGAACTCCCAAGAGANCGATGTGATGAATAATTCTGAAANCCATTTTGTGCCCCACTCATTGANAAGGANGGGG
TGNATCCTGTTTCTTCACTCCCTGNTGGAAAATGCTACAANCCCTGAACCAACCCATTTTCCCAANGAACCNNGNTGAAA
CCNTACCNNGGTTTNTTTTCCCTNAAACANCCCTCCCCTTTGGCCCCCGCGNTTNCGCTNCGGGNCCCNNAACCCNGG

N

27/30

seq13 rib31

NNTTNTCCTACGNCCTTTTAAANANAACCAGACCCCTCTGGANAATTANATNNCCACTGCTTACTGGCTTATCGAAATC
AATACGACTCACTATANGGAGACCCCAAGCTTACAGTCCCTGATGAGTCCGTGAGGACGAAAGGCTGAATCTANAGGGCCC
TATTCATAGTGTCACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCCTTCTAATTGCCAGCCATCTGTTGTTT
GCCCCCCCCGTCCTTCCCTTGACCCCTGGAAGTGCCACTCCCACTGTCTNTCCTAATAAAATGATGANNNTGCATCG
CATGTCTGAGTAAGTGTCAANTCTATTCTGGGGGTGGGTGGGCANGACANCAAGGGGAAGATTGGGAAAAACATTN
CACGCATGCCGGGGATGCGGTGGGTCTTNTTNGCNTCNGAAGCNGAAAAACNACTGGGGCCCTANGGGTNNCCCN
TCCCCNTGTAAACNGNCCTTNAACNCGGGGTTGTGGTTNNCCNANCTTANCNCTNAACTCCNNCCCCNNNCCCCCNC
TCTTCCCTTTTTCCTCCATCTCCNCNTTNNCCGNTCTCCCTTNCATNAATGGGGCCCCCTACNGGNCNTNTNTCT
CTTNNNNCCNCCNANANATATNCTNGNTNNTTCNCCCTCTCGGGCCCTCANNNCANNNTTCTCTNCNCANNNCCNC
CNNNCCACTCCCCCTTNCNTATCCCTNCATCTNNCTANAANCNTCNCCTCANNCCCTCNCCTANATANCNAANCCCTCN
CACCCCTTACACACNTCTTCCCCCTCTNNNNNCATCTCNTTCTTNCCTACCCNGNCTCCCCCTCNNCNTTCTACTCN
CTCANNNGTCTNCNNTCCCTCTNNNTNNACTNCCCTCTCTCTCNCNCCNCCNNTCNCCTCCCTCNNACCCCTNNTCGNCATC
NTNNNTTCTNCCCTNCTACNTCCCTNTNTCCCCNTTCTCNCNNCTCTNCTCTNTNNCACTCACCCCTCNCNGCTCNNCNTC
TCTTCTCNCNTCTCCCCC

28/30

seq14 PCR3 polcolla2

NTCNCGNCATTTAANCAGGCCAGGNCCTACCGCNCNGGTCCANGTAGGCCGGGAGCCCCAGCAACGCCGGGAAGGCCAGCAG
CACCCCTTGGCACCAAGTAAGGCCGTTTGCTCCAGGATTACCANGAGGTCCACGGGGCCGAGAGGCTGGAAANACCACTT
CACACGGGGAACCGCGGGTCCAGTAGGACCAGCGTTACCAACAGCTCCAATTTCAACCCTTGGGGCCAGGGGCACCTGG
GAAGCCTGGANGGCCAGCAGACCAATGGGACCAGCAGGACCCACGGACCACACTTCCATCACTGCTTTNGCNCAGCTGGGC
AAGGCACAACACTTCTCTCACANGAACCCACGGCTCCTGTTTNACTGAATCCATTTACAGGGCACAGTTCACCTT
CACACAAGAACACGGNTGTCCCTTCATCATCAGACATGTTCCCTAATGCTTGAGCAGANTCAGATTCAGGAAACACACAC
CTTTGTCCACATCTCTNCACAGTCTCGGTTTCAGGTACACTCCCCACCTGCAGAGGCACCTGACCAACCTGAGACATTGACA
TTNCAGNCCACAGCTGAAGTGAAGCGGGCAGCCATGGCNAAGTCATACCTGTCAAGNATCATCTTCTTANCAATCCCCAA
NGGGCAGAAATGAAAGCTGACTCCCCAATGTCTTATTTTAANNANGGTTTNAANAANNNNNNNNNNNNNNNNNNNNC
CCCCCCCCCTTNGGGTTTATTATCTATNCNCCCNCTNGGATATCTTNNCCCCCTTNCCTNAAANTTTTNTNTTTT
TNNNNNNNGGNTNNTTTTNNNNCCCNNTTTTNTTTTNNNGGGGNNTTT

29/30

seq15 tot polcolla2

CCCTTTAAACANGGCCAGGAATACCGCGGGGTCCAGGAGGCCGGACCCCANCAACGCCGGGAANGCCCAGCAGCACC
CTTGGCACCAAGTAAANGCCGTTTGCTCCAGGATTACCAGAGGTCCTCAACGGGGCCGGAGANGCCTGGAAAGACCACTTCACC
ACGGGAACGGCGGACCAAGCANGACAGCGTTACCAACAGCTCCAATTTCACCCCTTGGGGCCAGGGGCACCTGGGAAGC
CTGGANGGCCAGCAGACCAATGGGANCAAGCAGGACCAACGGGACCACTTCCATCNCCTGCCNCTGGCACCACTGGGCAA
GGCACAACACTTCTCTCACNAAGAACCCACGGNTCCTGTTAACTGAATTCCATTTCACAGGGCACAGTTCACCTTC
ANACAGAACACGGGTGTCCTTCATCATCAAAACATNTTCCCTATNCCTTGAGCAGAAATCAGATTCAGGAACACACACTTTC
TCACATCTCCTCACAGTCTCGGTTTCAGGTAACACTCNCACCTGCAGAGGCACCTGACNAANCTCAGANATTANATTCN
CTCCNCAGTTTGAACTTAGGCGGGCCCTNNCATTTGGNTTGTCCCTAACCTNTNGGGGTTTTCCTNNNNNNNNNNTTT
NACNANTCCCAANGGGGANAANAGNTGACTCCTATGTCCTTNTNTNAAAAGGTTTTTNAAAAAATAACCCCCCCCCCTN
TTGGGTTATTATTTTTTTNNCCCCCTTTTNGAANCNTNNCCCCNTTTTCCCCNNNAAANTTTTTTNTTTTTTTGNN
NNNNNTTGGGTTNNTTTNTNNCCCCNNTTTNNANTTNGGGGT

30/30

seq16 RIB908

NCTTTCNNCTNATNCAANAAGCAGGCCCTCTNNAAAACTANANTTCCACTGCTTACTGGCTTATCGAAANCAATAC
GACTCACTATAGGGAGACCCCAAGCTTCGGCGGCTGATGAGTCCGTGAGGACGAAACCAGCATCTAGAGGGCCCTATTCTA
TAGTGTCACCTAAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTGCCCCCTC
CCCCGTGCCCTTCCTTGACCCCTGGAAGTGCCACTCCCACTGTCTTCTCTAATAAAATGANGAAATTCATCGCATTTGTC
TGAGTANGTGTCACTTCTATCTGGGGGTGGGTGGGCGANGACANCAAGGGGAAAGATTGGGAANACAATAACAGGCAT
GCTGGGGATGCGGTGGCTCTATGGCTTCTGAGGCGGAAAGAACCAACTGGGCTCTANGGGGTATCCCCACNCCCCTGT
TACCGGCGCATTAANC GCGGGGTGTTGTGTTACCCNCAACTTAACGCTACACTTGCCACGCCCTAACGCCCTCCTTTC
GCTTCTTCCTTCTCCCACTTCCCCGNTTTCCTTCAACTCTAATCGGGCNCCTTAGGTCCAATTAATCTACGGN
CNCACCCAAAACCTNATAGGTAAGTCTTNTGGCCCCCCTAAAGTTCCCCCTAAATGAATCNNTCTAAATGAACNTTCNA
GGAACCCNCCCNCTNCTTAAANGAANNNNNCCCNNAAAAAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNAANCNNAATTTTNGGTGAACCCCCCGNAATTAANTCCNTTCNCTTTTTCCTCCCNANNNNNNNNTNNNN
NNNNNTCCNCCNNNNNNNNNCCNNTTTTNNNNCCNCCCNNAANANTTNGNNNNCCNCCNNTTTTAA
AAAAANNNAAAAAANCCNNGTNANNANAANAANNNTCTTTTNNNNCCCC

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